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30 OCT 2006

Allison C. Collard
Collard & Roe, P.C.
1077 Northern Boulevard
Roslyn, NY 11576

In re Application of	:	
BERHNARDT, et al.	:	DECISION ON RENEWED
Application No.: 10/512,737	:	
PCT No.: PCT/EP03/03973	:	PETITION UNDER
Int. Filing Date: 16 April 2003	:	
Priority Date: 29 April 2002	:	37 CFR 1.137(b)
Atty. Docket No.: BERNHARDT ET AL 2 PCT	:	
For: TRANSPORT SYSTEM IN BIOLOGICAL	:	
SYSTEMS	:	

This decision is in response to applicant's "Renewed Petition And Response to Decision on Petition Under 37 CFR 1.137 (b)" filed 29 September 2006 in the United States Patent and Trademark Office (USPTO).

The renewed petition to revive under 37 CFR 1.137(b) is hereby **DISMISSED** as follows:

As detailed in the decision mailed 17 August 2006, a petition under 37 CFR 1.137(b) requesting that the application be revived on the grounds of unintentional abandonment must be accompanied by (1) the required reply, (2) the petition fee required by law, (3) a statement that the, "entire delay in filing the required reply from the due date for the reply until the filing of a grantable petition pursuant to this paragraph was unintentional" and (4) any terminal disclaimer and fee pursuant to 37 CFR 1.137(c) (where required). Applicant previously satisfied items (2) - (4) above.

However, with regard to item (1), the proper response in the form of a compliant required sequence listing pursuant to 37 CFR 1.821-1.825 has still not been provided. The computer readable form filed 29 September 2006 was found to be non-compliant and a corrected diskette is needed. (See attached copy of CRF Problem Report.) Accordingly, the proper reply has not been furnished.

For the reasons stated above, the petition for revival cannot be granted at this time and the application remains abandoned.

CONCLUSION

Applicant's renewed petition under 37 CFR 1.137(b) is **DISMISSED**.

This application remains abandoned as to the United States of America.

If reconsideration on the merits of this petition is desired, a proper response must be filed within **TWO (2) MONTHS** from the mail date of this decision. Any reconsideration request should include a cover letter entitled "Renewed Petition Under 37 CFR 1.137(b)." No additional petition fee is required.

Please direct further correspondence with respect to this matter to the Mail Stop PCT, Commissioner for Patents, Office of PCT Legal Administration, P.O. Box 1450, Alexandria, Virginia 22313-1450, with the contents of the letter marked to the attention of the Office of PCT Legal Administration.



Derek A. Putonen
Attorney Advisor
Office of PCT Legal Administration
Tel: (571) 272-3294
Fax: (571) 273-0459

Encl: Copy of CRF Problem Report

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/512, 737B
Source: JFWP
Date Processed by STIC: 10/10/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**<http://www.uspto.gov/ebs/efs/downloads/documents.htm>**> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/512,737B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

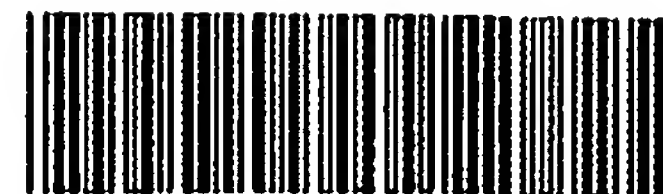
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

- 11 Use of <220> ~~Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules~~

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWP

RAW SEQUENCE LISTING

DATE: 10/10/2006

PATENT APPLICATION: US/10/512,737B

TIME: 14:47:03

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\10102006\J512737B.raw

2 <110> APPLICANT: BioTeSys GmbH
 3 Schelztorstrasse 54-56
 4 D 73728 Esslingen
 5 GERMANY
 W--> 6 <120> TITLE OF INVENTION: transport system in biological systems
 C--> 7 <140> CURRENT APPLICATION NUMBER: US/10/512,737B
 C--> 7 <141> CURRENT FILING DATE: 2004-10-27
 W--> 0 <130> FILE REFERENCE:
 7 <150> PRIOR APPLICATION NUMBER: A 656/2002
 8 <151> PRIOR FILING DATE: 2002-04-29
 W--> 9 <160> NUMBER OF SEQ ID: 15

Does Not Comply
 Corrected Diskette Needed

ERRORED SEQUENCES

84 <210> SEQ ID NO: 9
 85 <211> LENGTH: 22
 86 <212> TYPE: PRT
 87 <213> ORGANISM: Artificial sequence
 W--> 88 <220> FEATURE:
 89 <223> OTHER INFORMATION: Amino Acid
 W--> 90 <400> SEQUENCE: 9
 E--> 91 lie Val Ala Ile Leu Ile Cys Ile Leu Ile Leu Leu Thr Met Val Leu Leu Phe Val Met
 E--> 92 Trp Met
 E--> 93 1
 E--> 94 20

Invalid Response.
 What is the source of genetic material? See
 gleim non summary sheet.

Invalid Amino Acid Designator.

The type of errors shown exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/512,737B

DATE: 10/10/2006
TIME: 14:47:05

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\10102006\J512737B.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:9; Line(s) 91,93

Seq#:11; Line(s) 112

VERIFICATION SUMMARY

DATE: 10/10/2006

PATENT APPLICATION: US/10/512,737B

TIME: 14:47:05

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\10102006\J512737B.raw

L:6 M:283 W: Missing Blank Line separator, <120> field identifier
L:7 M:270 C: Current Application Number differs, Replaced Current Application No
L:7 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE
L:9 M:283 W: Missing Blank Line separator, <160> field identifier
L:10 M:283 W: Missing Blank Line separator, <210> field identifier
L:14 M:283 W: Missing Blank Line separator, <220> field identifier
L:16 M:283 W: Missing Blank Line separator, <400> field identifier
L:23 M:283 W: Missing Blank Line separator, <220> field identifier
L:33 M:283 W: Missing Blank Line separator, <220> field identifier
L:35 M:283 W: Missing Blank Line separator, <400> field identifier
L:42 M:283 W: Missing Blank Line separator, <220> field identifier
L:44 M:283 W: Missing Blank Line separator, <400> field identifier
L:51 M:283 W: Missing Blank Line separator, <220> field identifier
L:53 M:283 W: Missing Blank Line separator, <400> field identifier
L:60 M:283 W: Missing Blank Line separator, <220> field identifier
L:62 M:283 W: Missing Blank Line separator, <400> field identifier
L:69 M:283 W: Missing Blank Line separator, <220> field identifier
L:71 M:283 W: Missing Blank Line separator, <400> field identifier
L:79 M:283 W: Missing Blank Line separator, <220> field identifier
L:81 M:283 W: Missing Blank Line separator, <400> field identifier
L:88 M:283 W: Missing Blank Line separator, <220> field identifier
L:90 M:283 W: Missing Blank Line separator, <400> field identifier
L:91 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:92 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
M:332 Repeated in SeqNo=9
L:99 M:283 W: Missing Blank Line separator, <220> field identifier
L:101 M:283 W: Missing Blank Line separator, <400> field identifier
L:108 M:283 W: Missing Blank Line separator, <220> field identifier
L:110 M:283 W: Missing Blank Line separator, <400> field identifier
L:117 M:283 W: Missing Blank Line separator, <220> field identifier
L:119 M:283 W: Missing Blank Line separator, <400> field identifier
L:126 M:283 W: Missing Blank Line separator, <220> field identifier
L:128 M:283 W: Missing Blank Line separator, <400> field identifier
L:135 M:283 W: Missing Blank Line separator, <220> field identifier
L:137 M:283 W: Missing Blank Line separator, <400> field identifier
L:144 M:283 W: Missing Blank Line separator, <220> field identifier
L:146 M:283 W: Missing Blank Line separator, <400> field identifier